

SUPPLEMENTAL PRELIMINARY AMENDMENT
U.S. Appln. No. 10/727,576

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claims 1-17. (Cancelled).

Claim 18. (New) A method of obtaining isolated selected mRNA species or isolated selected cDNA species useful for diagnosing or identifying cancer or a stage thereof in a eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells from blood of one or more eukaryotic organisms which are known to have cancer or a stage thereof (cancer sample), wherein said cells have not contacted the area of said cancer and said blood is obtained from a part of said organism distant to the area of said cancer, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells from blood of one or more corresponding normal eukaryotic organisms (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subject to reverse transcription to obtain separated cDNA species;

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- (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c), respectively, which are present at a different level in the normal sample than in the cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species; and
- (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species.

Claim 19. (New) A method of preparing a gene transcript pattern probe kit comprising the steps of:

- (a) isolating mRNA from cells from blood of one or more eukaryotic organisms which are known to have cancer or a stage thereof (cancer sample), wherein said cells have not contacted the area of said cancer and said blood is obtained from a part of said organism distant to the area of said cancer, wherein the resulting isolated mRNA is

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- optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells from blood of one or more corresponding normal eukaryotic organisms (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
 - (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subject to reverse transcription to obtain separated cDNA species;
 - (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c) respectively, which are present at a different level in the normal sample than in the cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species;
 - (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected

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mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species; and

- (f) immobilizing the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) on at least one solid support so as to form a gene transcript pattern probe kit.

Claim 20. (New) The method as claimed in claim 18 or 19, wherein said separation in step (c) is performed by a non-sequence based separation technique.

Claim 21. (New) The method as claimed in claim 18 or 19, wherein in steps (a) and (b), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

Claim 22. (New) The method as claimed in claim 21, wherein said isolated cDNA is amplified.

Claim 23. (New) The method as claimed in claim 18 or 19, wherein in step (e), between 50 and 100 mRNA species or cDNA species are isolated and selected.

Claim 24. (New) The method as claimed in claim 18 or 19, wherein, in step (e) between 10 and 500 mRNA species or cDNA species are isolated and selected.

Claim 25. (New) The method as claimed in claim 18 or 19, wherein, in step (c), said separation technique is gel electrophoresis.

Claim 26. (New) The method as claimed in claim 19, wherein, prior to immobilizing in step (f), the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) are amplified.

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Claim 27. (New) A method of preparing a standard gene transcript pattern characteristic of cancer or a stage thereof of a eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells from blood of one or more eukaryotic organisms known to have said cancer or a stage thereof (cancer sample), wherein said blood is obtained from a part of said organism distant to the area of said cancer, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from one or more normal eukaryotic organisms than in corresponding cells in a blood sample from one or more eukaryotic organisms known to have said cancer or a stage thereof, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said cancer or stage thereof and wherein said cells have not contacted the area of said cancer and said blood is obtained from a part of said organism distant to the area of said cancer, wherein said mRNA or cDNA species are immobilized on a solid support; and
- (c) assessing the amount of hybridization so as to obtain said standard gene transcript pattern.

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Claim 28. (New) A method of preparing a test gene transcript pattern for cancer or a stage thereof comprising the steps of:

- (a) isolating mRNA from cells from blood of a test eukaryotic organism, wherein said blood is obtained from a part of said organism distant to the area of said cancer, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from one or more normal eukaryotic organisms than in corresponding cells in a blood sample from one or more eukaryotic organisms known to have said cancer or a stage thereof, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said cancer or stage thereof and wherein said cells have not contacted the area of said cancer and said blood is obtained from a part of said organism distant to the area of said cancer, wherein said mRNA or cDNA species are immobilized on a solid support; and
- (c) assessing the amount of hybridization so as to obtain said test gene transcript pattern.

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Claim 29. (New) A method of diagnosing or identifying cancer or a stage thereof in a test eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells from blood of a test eukaryotic organism, wherein said blood is obtained from a part of said organism distant to the area of said cancer, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from one or more normal eukaryotic organisms than in corresponding cells in a blood sample from one or more eukaryotic organisms known to have said cancer or a stage thereof, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said cancer or stage thereof and wherein said cells have not contacted the area of said cancer and said blood is obtained from a part of said organism distant to the area of said cancer, wherein said mRNA or cDNA species are immobilized on a solid support;
- (c) assessing the amount of hybridization so as to obtain a hybridization pattern; and
- (d) comparing the resulting hybridization pattern obtained in step (c) with a hybridization pattern

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obtained by hybridizing isolated mRNA or isolated cDNA prepared from corresponding cells from blood of one or more corresponding eukaryotic organisms known to have said cancer or stage thereof to the 10 or more mRNA species or 10 or more cDNA species transcribed from said mRNA species, wherein said mRNA species or cDNA species are immobilized on a solid support, so as to determine the degree of correlation indicative of the presence of said cancer or stage thereof, and so as to diagnose or identify said cancer or a stage thereof in said test eukaryotic organism.

Claim 30. (New) The method as claimed in claim 27, 28 or 29, wherein in step (a), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

Claim 31. (New) The method as claimed in claim 30, wherein said isolated cDNA is amplified.

Claim 32. (new) The method as claimed in claim 18, 19, 27, 28 or 29, wherein said isolated cDNA is labeled.

Claim 33. (New) The method as claimed in claim 27, 28 or 29, wherein, in step (b), between 50 and 100 mRNA species or cDNA species are used.

Claim 34. (New) The method as claimed in claim 27, 28 or 29, wherein, in step (b), between 10 and 500 mRNA species or cDNA species are used.

Claim 35. (New) The method as claimed in claim 19, 27, 28 or 29, wherein said solid support is a filter.

Claim 36. (New) The method as claimed in claim 18, 19, 27, 28 or 29, wherein said organism is human.

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Claim 37. (New) The method as claimed in claim 18, 19, 27, 28 or 29, wherein said cancer is selected from the group comprising stomach, lung, breast, prostate gland, bowel and skin cancer.

Claim 38. (New) The method as claimed in claim 18, 19, 27, 28 or 29, wherein said cancer is breast cancer.